Neutrokine-α

```
1    AAATTCAGGATAACTCTCCTGAGGGGTGAGCCAAGCCCTGCCATGTAGTGCACGCAGGAC  60

61   ATCAACAAACACAGATAACAGGAAATGATCCATTCCCTGTGGTCACTTATTCTAAAGGCC  120

121  CCAACCTTCAAAGTTCAAGTAGTGATATGGATGACTCCACAGAAAGGGAGCAGTCACGCC  180
1                              M  D  D  S  T  E  R  E  Q  S  R  L   12

181  TTACTTCTTGCCTTAAGAAAAGAGAAGAAATGAAACTGAAGGAGTGTGTTTCCATCCTCC  240
13    T  S  C  L  K  K  R  E  E  M  K  L  K  E  C  V  S  I  L  P   32
                                                          CD-I

241  CACGGAAGGAAAGCCCCTCTGTCCGATCCTCCAAAGACGGAAAGCTGCTGGCTGCAACCT  300
33    R  K  E  S  P  S  V  R  S  S  K  D  G  K  L  L  A  A  T  L   52
                  CD-I

301  TGCTGCTGGCACTGCTGTCTTGCTGCCTCACGGTGGTGTCTTTCTACCAGGTGGCCGCCC  360
53    L  L  A  L  L  S  C  C  L  T  V  V  S  F  Y  Q  V  A  A  L   72

361  TGCAAGGGGACCTGGCCAGCCTCCGGGCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGC  420
73    Q  G  D  L  A  S  L  R  A  E  L  Q  G  H  H  A  E  K  L  P   92
                  CD-II

421  CAGCAGGAGCAGGAGCCCCCAAGGCCGGCCTGGAGGAAGCTCCAGCTGTCACCGCGGGAC  480
93    A  G  A  G  A  P  K  A  G  L  E  E  A  P  A  V  T  A  G  L  112
                  CD-III

                                    #
481  TGAAAATCTTTGAACCACCAGCTCCAGGAGAAGGCAACTCCAGTCAGAACAGCAGAAATA  540
113   K  I  F  E  P  P  A  P  G  E  G  N  S  S  Q  N  S  R  N  K  132

541  AGCGTGCCGTTCAGGGTCCAGAAGAAACAGTCACTCAAGACTGCTTGCAACTGATTGCAG  600
133   R  A  V  Q  G  P  E  E  T  V  T  Q  D  C  L  Q  L  I  A  D  152
                                                          CD-IV
```

FIG.1A

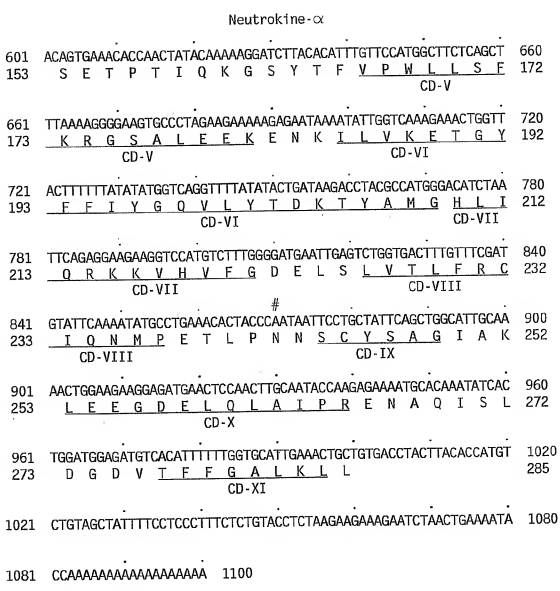
Neutrokine-α
601 ACAGTGAAACACCAACTATACAAAAAGGATCTTACACATTTGTTCCATGGCTTCTCAGCT 660
153 S E T P T I Q K G S Y T F V P W L L S F 172
CD-V
661 TTAAAAGGGGAAGTGCCCTAGAAGAAAAAGAGAATAAAATATTGGTCAAAGAAACTGGTT 720
173 K R G S A L E E K E N K I L V K E T G Y 192
CD-V
CD-VI
721 ACTTTTTTATATATGGTCAGGTTTTATATACTGATAAGACCTACGCCATGGGACATCTAA 780
193 F F I Y G Q V L Y T D K T Y A M G H L I 212
CD-VI
CD-VII
781 TTCAGAGGAAGAAGGTCCATGTCTTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGAT 840
213 Q R K K V H V F G D E L S L V T L F R C 232
CD-VII
CD-VIII
#
841 GTATTCAAAATATGCCTGAAACACTACCCAATAATTCCTGCTATTCAGCTGGCATTGCAA 900
233 I Q N M P E T L P N N S C Y S A G I A K 252
CD-VIII
CD-IX
901 AACTGGAAGAAGGAGATGAACTCCAACTTGCAATACCAAGAGAAAATGCACAAATATCAC 960
253 L E E G D E L Q L A I P R E N A Q I S L 272
CD-X
961 TGGATGGAGATGTCACATTTTTTGGTGCATTGAAACTGCTGTGACCTACTTACACCATGT 1020
273 D G D V T F F G A L K L L 285
CD-XI
1021 CTGTAGCTATTTTCCTCCCTTTCTCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATA 1080
1081 CCAAAAAAAAAAAAAAAAA 1100

FIG.1B

```
                 10        20        30
1  MSTESMIRDVEL--------------AEEA  TNFalpha
1  M-----------------------TPPERL  TNFbeta
1  MGA---------------------------  LTbeta
1  MQQPFNYPYPQIYW-VDSSASSPWAPPGTV  FasLigand
1  MDDSTEREQSRLTSCLKKREEMKLKECVSI  Neutrokine alpha
1  MDDSTEREQSRLTSCLKKREEMKLKECVSI  Neutrokine alphaSV

           40        50        60
17 LPKKTGGPQ--GSRR---------------  TNFalpha
8  F-----------------------------  TNFbeta
4  ----LGLEGRGG------------------  LTbeta
30 LPCPTSVPRRPGQRRPPPPPPPPPLPPPPP  FasLigand
31 LPRKESPSVRSSKD---GKLLAATLLLALL  Neutrokine alpha
31 LPRKESPSVRSSKD---GKLLAATLLLALL  Neutrokine alphaSV

           70        80        90
30 ----------------------CLFLSLFS  TNFalpha
9  --------LPRVRGTTLHLLLLGLLLVLLP  TNFbeta
12 ----------RLQGRGSLLLAVAGATSLVT  LTbeta
60 PPPLPPLPLPPLKKRGNHSTGLCLLVMFFM  FasLigand
58 SCCLTVVSFYQVAALQGDLASLRAELQGHH  Neutrokine alpha
58 SCCLTVVSFYQVAALQGDLASLRAELQGHH  Neutrokine alphaSV
```

FIG.2A

```
                        100       110       120
38   FL--IVAGATTLFCLLHFGVIGPQREEFPR   TNFalpha
31   GAQGLPGVGL--------------------   TNFbeta
32   LLLAVPITVLAVLALVPQDQGGLVTETADP   LTbeta
90   VLVALVGLGLGMFQLFHLQKELAELRESTS   FasLigand
88   AEKLPAGAGAPKAGLEEAPAVTAGLKIFEP   Neutrokine alpha
88   AEKLPAGAGAPKAGLEEAPAVTAGLKIFEP   Neutrokine alphaSV

                        130       140       150
66   DLSLIS-PLA-QAVRSSSRTPSD---KPVA   TNFalpha
41   ---TPS-AAQ-TARQHPKMHLAHSTLKPAA   TNFbeta
62   GAQAQQ-GLGFQKLPEEEPETDLSPGLPAA   LTbeta
120  QMHTAS-SLE-KQIGHPSPPPEKKELRKVA   FasLigand
118  PAPGEGNSSQNSRNKRAVQGPEETVTQDCL   Neutrokine alpha
118  PAPGEGNSSQNSRNKRAVQGPEET------   Neutrokine alphaSV

                        160       170       180
91   HVVANPQAEG-Q------LQWLNRRANALL   TNFalpha
66   HLIGDPSKQN-S------LLWRANTDRAFL   TNFbeta
91   HLIGAPLK-GQG------LGWETTKEQAFL   LTbeta
148  HLTGKSNSRSMP------LEWEDIYGIVLL   FasLigand
148  QLIADSETPTIQKGSYTFVPWL----LSFK   Neutrokine alpha
142  -------------GSYTFVPWL----LSFK   Neutrokine alphaSV
```

FIG.2B

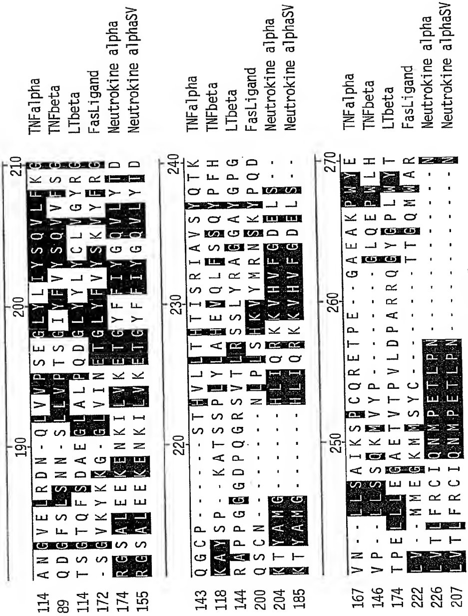
TNFalpha
TNFbeta
LTbeta
FasLigand
Neutrokine alpha
Neutrokine alphaSV

FIG.2C

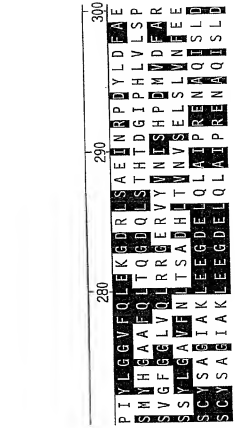
280
290
300
310
193 P I Y L G G V F Q L E K G D R L S A E I N R P D Y L D F A E TNFalpha
166 S M H L A F Q N T Q G D L S T H T D G I P H L V L S P TNFbeta
204 S V G F G G L V K L R R G S G S E R V Y G N L S H P D M D F A R LTbeta
242 S S Y L G A F N L T S A D H L F V S V L S S Q F L R A I E E L E FasLigand
244 S C Y S A G I A K L E E G D E L Q L A I P R E N A Q I S L D G Neutrokine alpha
225 S C W S A G I A K L E E G D E L Q L A I P R E N A Q I S L D G Neutrokine alphaSV
223 S C Q V Y F G I I A L TNFalpha
196 S L T V F F G A F A L TNFbeta
234 - C K T F F G A V M V G LTbeta
272 - S Q T F F G L Y K L FasLigand
274 G D V T F F G A L K L Neutrokine alpha
255 G D V T F F G A L K L Neutrokine alphaSV

FIG.2D

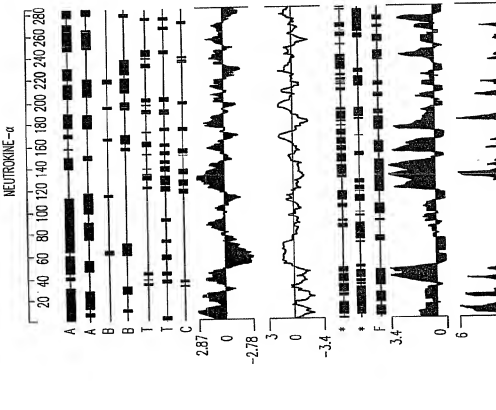
NEUTROKINE-α
20 40 60 80 100 120 140 160 180 200 220 240 260 280
A
A
B
B
T
T
C
2.87
0
-2.78
3
0
-3.4
*
*
F
3.4
0
6
1
■ ALPHA, REGIONS-GARNIER-ROBSON
■ ALPHA, REGIONS-CHOU-FASMAN
■ BETA, REGIONS-GARNIER-ROBSON
■ BETA, REGIONS-CHOU-FASMAN
■ TURN, REGIONS-GARNIER-ROBSON
■ TURN, REGIONS-CHOU-FASMAN
■ COIL, REGIONS-GARNIER-ROBSON
■ HYDROPHILICITY PLOT-KYTE-DOOLITTLE
□ HYDROPHOBICITY PLOT-HOPP-WOODS
■ ALPHA, AMPHIPATHIC REGIONS-EISENBERG
■ BETA, AMPHIPATHIC REGIONS-EISENBERG
■ FLEXIBLE REGIONS-KARPLUS-SCHULZ
■ ANTIGENIC INDEX-JAMESON-WOLF
■ SURFACE PROBABILITY PLOT-EMINI

FIG.3

```
                1                                                    50
HSOAD55R  .........A GGNTAACTCT CCTGAGGGGT GAGCCAAGCC CTGCCATGTA
HNEDU15X  ...AAATTCA GGATAACTCT CCTGAGGGGT GAGCCAAGCC CTGCCATGTA
HSLAH84R  .AATTCGGCA NAGNAAACTG GTTACTTTTT TATATATGGT CAGGTTTTAT
HLTBM08R  AATTCGGCAC GAGCAAGGCC GGCCTGGAGG AAGCTCCAGC TGTCACCGCG

               51                                                   100
HSOAD55R  GTGCACGCAG GACATCANCA A..ACACANN NNNCAGGAAA TAATCCATTC
HNEDU15X  GTGCACGCAG GACATCAACA A..ACACAGA TAACAGGAAA TGATCCATTC
HSLAH84R  ATACTGATAA GACCTACGCC ATGGGACATC TAGTTCAGAG GAAGAAGGTC
HLTBM08R  GGACTGAAAA TCTTTGAACC ACCAGCTCCA GGAGAAGGCA ACTCCAGTCA

              101                                                   150
HSOAD55R  CCTGTGGTCA CTTATTCTAA AGGCCCCAAC CTTCAAAGTT CAAGTAGTGA
HNEDU15X  CCTGTGGTCA CTTATTCTAA AGGCCCCAAC CTTCAAAGTT CAAGTAGTGA
HSLAH84R  CATGTCTTTG GGGATGAATT GAGTCTGGTG ACTTTGTTTC GATGTATTCA
HLTBM08R  GAACAGCAGA AATAAGCGTG CCGTTCAGGG TCCAGAAGAA ACAGTCACTC

              151                                                   200
HSOAD55R  TATGGATGAC TCCACAGAAA GGGAGCAGTC ACGCCTTACT TCTTGCCTTA
HNEDU15X  TATGGATGAC TCCACAGAAA GGGAGCAGTC ACGCCTTACT TCTTGCCTTA
HSLAH84R  AAATATGCCT GAAACACTAC CCAATAATTC CTGCTATTCA GCTGGCATTG
HLTBM08R  AAGACTGCTT GCAACTGNTT GCAGACAGTG AAACACCAAC TATACAAAAA

              201                                                   250
HSOAD55R  AGAAAAGAGA AGAAATGAAA CTGNAAGGAG TGTGTTTCCA TCCTCCCACG
HNEDU15X  AGAAAAGAGA AGAAATGAAA CT.GAAGGAG TGTGTTTCCA TCCTCCCACG
HSLAH84R  CAAAACTGGN AGGAAGGA.. ...GATGAAC TCCAACTTGC AATACCAGGG
HLTBM08R  GGCTCCCTTC TGNTGCCACA TTTGGGCCAA GGAATGGAGA GATTTCTTCG

              251                                                   300
HSOAD55R  GAAGGAAAGC CCCTCTNTCC GATCCTCCAA AGACGGAAAG CTGCTGGCTG
HNEDU15X  GAAGGAAAGC CCCTCTGTCC GATCCTCCAA AGACGGAAAG CTGCTGGCTG
HSLAH84R  GAAAATGCAC AATTATCACT GGGATGGAGA TGTTCACATT TTTTGGGTGC
HLTBM08R  TCTGGAAACA TTTTGCCAAA CTCTTCAGAT ACTCTTTNCT CTCTGGGAAT

              301                                                   350
HSOAD55R  CAACCTTGNT GNTGGCATTG TGTTCTTGCT GNCTCAAGGT GGTGTTNTT.
HNEDU15X  CAACCTTGCT GCTGGCACTG CTGTCTTGCT GCCTCACGGT GGTGTCTTTC
HSLAH84R  CATTGAAACT GCTGTGACCT NCTTACANCA NGTGCTGTTN GCTATTTTNC
HLTBM08R  CAAAGGAAAA TCTCTACTTA GATTNACACA TTTGTTCCCA TGGGTNTCTT

              351                                                   400
HSOAD55R  ......... ......... ......... ......... .........
HNEDU15X  TACCAGGTGG CCGCCCTGCA AGGGGACCTG GCCAGCCTCC GGGCAGAGCT
HSLAH84R  CTNCCTNTTC TNTGGTAACC TCTTAGGAAG GAAGGATTCT TAACTGGGAA
HLTBM08R  AAGTTTTAAA AGGGGAGTGC CCTTAGGAGG AAAAGGGGAT AAATATTGGC
```

FIG.4A

```
            401                                                        450
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    GCAGGGCCAC CACGCGGAGA AGCTGCCAGC AGGAGCAGGA GCCCCCAAGG
HSLAH84R    ATAACCCAAA AAAANTTAA ANGGGTANGN GNNANANGNG GGGNNGTTNN
HLTBM08R    CAAGGNACTG GTTANTTTNT AAATATGGTC AGGTTTNTAT ANCTGGTAGG

            451                                                        500
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    CCGGCCTGGA GGAAGCTCCA GCTGTCACCG CGGGACTGAA AATCTTTGAA
HSLAH84R    CNNGNNGNNT TTTNGGNNTA TNTTNTNNTN GGGNNNNGTA AAAATGGGGC
HLTBM08R    CCTCGCCATG GGCATTNATT CANGGNGAGG NCNNTCTTTT GGGNTGA...

            501                                                        550
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    CCACCAGCTC CAGGAGAAGG CAACTCCAGT CAGAACAGCA GAAATAAGCG
HSLAH84R    CNANGGGGGN TTTTT..... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            551                                                        600
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    TGCCGTTCAG GGTCCAGAAG AAACAGTCAC TCAAGACTGC TTGCAACTGA
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            601                                                        650
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    TTGCAGACAG TGAAACACCA ACTATACAAA AAGGATCTTA CACATTTGTT
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            651                                                        700
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    CCATGGCTTC TCAGCTTTAA AAGGGGAAGT GCCCTAGAAG AAAAAGAGAA
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            701                                                        750
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    TAAAATATTG GTCAAAGAAA CTGGTTACTT TTTTATATAT GGTCAGGTTT
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            751                                                        800
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    TATATACTGA TAAGACCTAC GCCATGGGAC ATCTAATTCA GAGGAAGAAG
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........
```

FIG.4B

```
            801                                                       850
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    GTCCATGTCT TTGGGGATGA ATTGAGTCTG GTGACTTTGT TTCGATGTAT
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            851                                                       900
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    TCAAAATATG CCTGAAACAC TACCCAATAA TTCCTGCTAT TCAGCTGGCA
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            901                                                       950
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    TTGCAAAACT GGAAGAAGGA GATGAACTCC AACTTGCAAT ACCAAGAGAA
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            951                                                      1000
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    AATGCACAAA TATCACTGGA TGGAGATGTC ACATTTTTTG GTGCATTGAA
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            1001                                                     1050
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    ACTGCTGTGA CCTACTTACA CCATGTCTGT AGCTATTTTC CTCCCTTTCT
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            1051                                                     1100
HSOAD55R    .......... .......... .......... .......... ..........
HNEDU15X    CTGTACCTCT AAGAAGAAAG AATCTAACTG AAAATACCAA AAAAAAAAA
HSLAH84R    .......... .......... .......... .......... ..........
HLTBM08R    .......... .......... .......... .......... ..........

            1101
HSOAD55R    ......
HNEDU15X    AAAAA
HSLAH84R    ......
HLTBM08R    ......
```

FIG.4C

Neutrokine-αSV

```
1   ATGGATGACTCCACAGAAAGGGAGCAGTCACGCCTTACTTCTTGCCTTAAGAAAAGAGAA  60
1   M  D  D  S  T  E  R  E  Q  S  R  L  T  S  C  L  K  K  R  E   20

61  GAAATGAAACTGAAGGAGTGTGTTTCCATCCTCCCACGGAAGGAAAGCCCCTCTGTCCGA  120
21  E  M  K  L  K  E  C  V  S  I  L  P  R  K  E  S  P  S  V  R   40
                                   CD-I

121 TCCTCCAAAGACGGAAAGCTGCTGGCTGCAACCTTGCTGCTGGCACTGCTGTCTTGCTGC  180
41  S  S  K  D  G  K  L  L  A  A  T  L  L  L  A  L  L  S  C  C   60
       CD-I

181 CTCACGGTGGTGTCTTTCTACCAGGTGGCCGCCCTGCAAGGGGACCTGGCCAGCCTCCGG  240
61  L  T  V  V  S  F  Y  Q  V  A  A  L  Q  G  D  L  A  S  L  R   80
                                      CD-II

241 GCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGCCAGCAGGAGCAGGAGCCCCAAGGCC  300
81  A  E  L  Q  G  H  H  A  E  K  L  P  A  G  A  G  A  P  K  A   100
       CD-II                                  CD-III

301 GGCCTGGAGGAAGCTCCAGCTGTCACCGCGGGACTGAAAATCTTTGAACCACCAGCTCCA  360
101 G  L  E  E  A  P  A  V  T  A  G  L  K  I  F  E  P  P  A  P   120
    CD-III
          #
361 GGAGAAGGCAACTCCAGTCAGAACAGCAGAAATAAGCGTGCCGTTCAGGGTCCAGAAGAA  420
121 G  E  G  N  S  S  Q  N  S  R  N  K  R  A  V  Q  G  P  E  E   140

421 ACAGGATCTTACACATTTGTTCCATGGCTTCTCAGCTTTAAAAGGGGAAGTGCCCTAGAA  480
141 T  G  S  Y  T  F  V  P  W  L  L  S  F  K  R  G  S  A  L  E   160
                                   CD-IV

481 GAAAAAGAGAATAAAATATTGGTCAAAGAAACTGGTTACTTTTTTATATATGGTCAGGTT  540
161 E  K  E  N  K  I  L  V  K  E  T  G  Y  F  F  I  Y  G  Q  V   180
    CD-IV                          CD-V

541 TTATATACTGATAAGACCTACGCCATGGGACATCTAATTCAGAGGAAGAAGGTCCATGTC  600
181 L  Y  T  D  K  T  Y  A  M  G  H  L  I  Q  R  K  K  V  H  V   200
             CD-VI                          CD-VII
```

FIG.5A

Neutrokine-αSV

```
601 TTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGATGTATTCAAAATATGCCTGAAACA 660
201 F G D E L S L V T L F R C I Q N M P E T 220
    CD-VIII          CD-VIII

661 CTACCCAATAATTCCTGCTATTCAGCTGGCATTGCAAAACTGGAAGAAGGAGATGAACTC 720
221 L P N N S C Y S A G I A K L E E G D E L 240
          CD-IX              CD-X

721 CAACTTGCAATACCAAGAGAAAATGCACAAATATCACTGGATGGAGATGTCACATTTTTT 780
241 Q L A I P R E N A Q I S L D G D V T F F 260
      CD-X                          CD-XI

781 GGTGCATTGAAACTGCTGTGACCTACTTACACCATGTCTGTAGCTATTTTCCTCCCTTTC 840
261 G A L K L L                                                  266
      CD-XI

841 TCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATACCAAAAAAAAAAAAAAAAAAAAA 900

901 AAA 903
```

FIG.5B

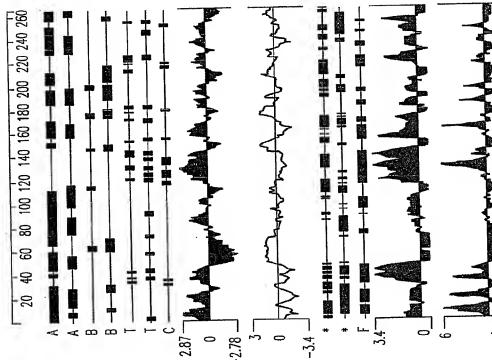
NEUTROKINE-αSV
20 40 60 80 100 120 140 160 180 200 220 240 260
A
A
B
B
T
T
C
2.87
0
-2.78
3
0
-3.4
*
*
F
3.4
0
6
1
ALPHA, REGIONS-GARNIER-ROBSON
ALPHA, REGIONS-CHOU-FASMAN
BETA, REGIONS-GARNIER-ROBSON
BETA, REGIONS-CHOU-FASMAN
TURN, REGIONS-GARNIER-ROBSON
TURN, REGIONS-CHOU-FASMAN
COIL, REGIONS-GARNIER-ROBSON
HYDROPHILICITY PLOT-KYTE-DOOLITTLE
HYDROPHOBICITY PLOT-HOPP-WOODS
ALPHA, AMPHIPATHIC REGIONS-EISENBERG
BETA, AMPHIPATHIC REGIONS-EISENBERG
FLEXIBLE REGIONS-KARPLUS-SCHULZ
ANTIGENIC INDEX-JAMESON-WOLF
SURFACE PROBABILITY PLOT-EMINI

FIG.6

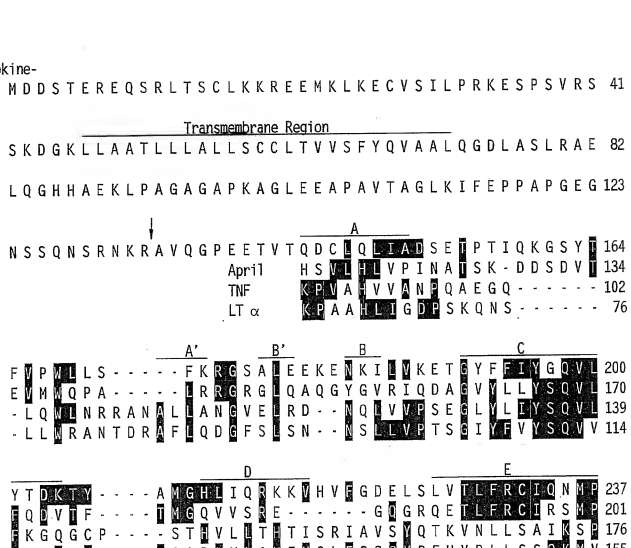
Neutrokine-
Alpha MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRS 41
Transmembrane Region
SKDGKLLAATLLLALLSCCLTVVSFYQVAALQGDLASLRAE 82
LQGHHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAPGEG 123
A
NSSQNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYT 164
April HSVLHLVPINATSK-DDSDVT 134
TNF KPVAHVVANPQAEGQ------ 102
LT α KPAAHLIGDPSKQNS------ 76
A' B' B C
FVPMLLS-----FKRGSALEEKENKILVKETGYFFIYGQVL 200
EVMQPA-----LRRGRGLQAQGYGVRIQDAGVYLLYSQVL 170
-LQWLNRRANALLANGVELRDN-NQLVVPSEGLYLIYSQVL 139
-LLNRANTDRAFLQDGFSLSN--NSLLVPTSGIYFVYSQVV 114
D E
YTDKTY----AMGHLIQRKKVHVFGDELSLVTLFRCIQNMP 237
FQDVTF----TMGQVVSRE------GQGRQETLFRCIRSMP 201
FKGQGCP----STHVLLTHTISRIAVSYQTKVNLLSAIKSP 176
FSGKAYSPKATSSPLYLAYEVQLFSSQYPFHVPLLSSQKMV 155

FIG.7A-1

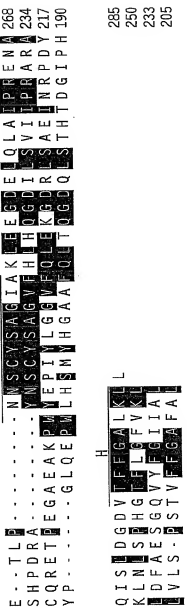
E--TL-------NWSCYSAGIAKLEGDELQLAIPRENA 268
SHPDRA------YWSCYSAGWFHLHGDLISVIIPRARA 234
CQRETGAEAKPWYEPILGCWFQLEKGDRLSAEINRPDY 217
YP---GLQEPWLHSMYHGAAFQLTQGQLSTHTDGIPH 190
F
G
H
QISLDGDVTFFGALKLL 285
KLNSHGTLFLGFVKIL 250
IDFAESGQVYFGIAIL 233
LVLS-STVFFGAFAI 205

FIG.7A-2

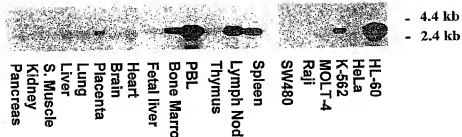
- 4.4 kb
- 2.4 kb
HL-60
HeLa
K-562
MOLT-4
Raji
SW480
Spleen
Lymph Node
Thymus
PBL
Bone Marrow
Fetal liver
Heart
Brain
Placenta
Lung
Liver
S. Muscle
Kidney
Pancreas

FIG.7B

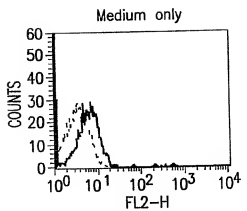

FIG.8A

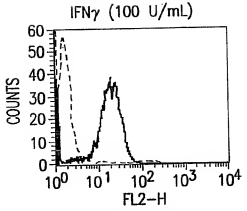

FIG.8B

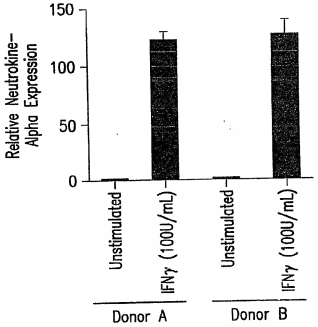

FIG.8C

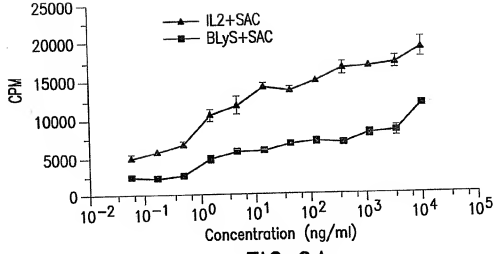
IL2+SAC
BLyS+SAC
CPM
25000
20000
15000
10000
5000
0
10^{-2} 10^{-1} 10^{0} 10^{1} 10^{2} 10^{3} 10^{4} 10^{5}
Concentration (ng/ml)

FIG. 9A

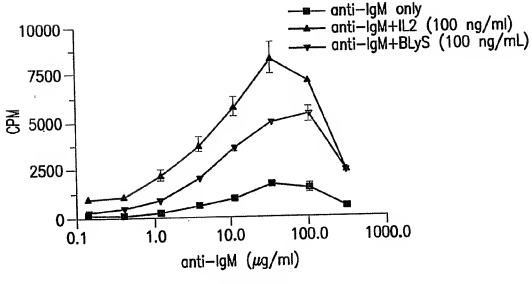
anti-IgM only
anti-IgM+IL2 (100 ng/ml)
anti-IgM+BLyS (100 ng/mL)
CPM
10000
7500
5000
2500
0
0.1
1.0
10.0
100.0
1000.0
anti-IgM (μg/ml)

FIG. 9B

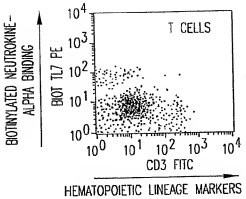

FIG.10A

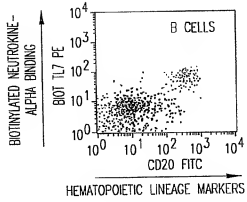

FIG.10B

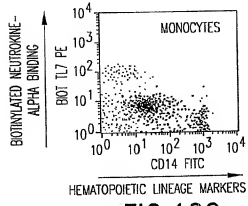

FIG.10C

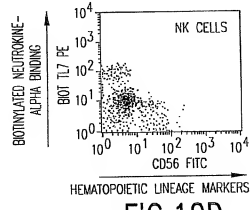

FIG.10D

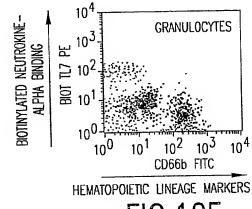

FIG.10E

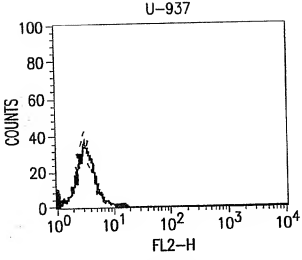

FIG.10F

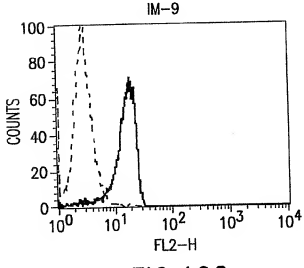

FIG.10G

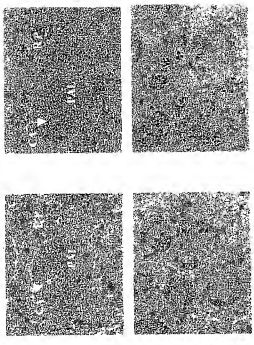
Normal spleen
Neutrokine - alpha treated spleen (2mg/Kg) bid 4d
H & E (100X)
CD45R(B220) (40X)

FIG. 11A

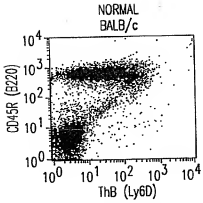

FIG. 11B

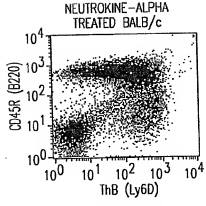

FIG. 11C

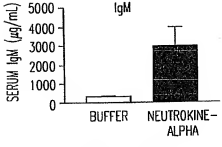

FIG. 11D

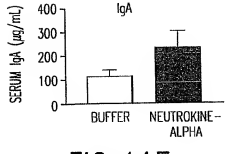

FIG. 11E

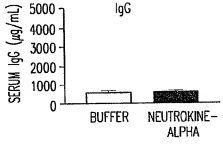

FIG. 11F